

FIG. 1

ATGTTCTTCTACTTCATTTCATCGTTCTGATCAATGTCAAAGATTTCGACTGACTCAA
GGTAGCATGATCACTCCCTCATGCCAAAAGGATATTTCCTGTGGGAATCTTACCAAG
TGCTTACCCGAGCTTTCACTGTGATGGAAGGATGACTGTGGGAACGGGCGGACGAA
GAGAACTGTGGTGCACACTGTGGATGGCGACCATATTGGCACAGTGCATGGAAATGCT
AACAGCGTGGCTTAAACAGGAGTCCTCTAAACAGTATCACAATGCTGTGACTGC
AAAGAAACTGAATTGGAAATGTGTAATGACTTAAAGCTGTGCCGATGATTCTAAC
AAITGTGACATTACTGTCTCTTAAGAAAAAAACATTCACAGCTCTCCAGATAAAGTTTC
ATCAAAACACAAAACCTTAAAGGATATTCTTCAGCATATACTGATTAGACACATATCC
AGGAAAGCATTTTGGATTGTAAATCTGAAATATTATCTCAACCCAACTGCATC
ACACCCCTAGACCTGGAAATTCAAAAGACTTACAGCTAACTTGGTAATTCTAGAT
GACAATCCAATAACAGAAATTTCACAGCGCTGTTACGGGATAATTCTGTTTTCT
CTGCTATGTTAATACTAGAGCTTCCAAAGCAGATGTGCCCCAAATGCGT
CAACTCAACTGGGATTGGAATTGGAAGGAACTAGATAAAGTCTCACAAATTCTACGTT
CTGTCGCGATTGCGTCAAGTGTGTTCTGCTGAGAAATCAAAATTGGTTTGTCCA
GAGAAGACATTCTGCTTCAATTAAAGGATTTAGGAAACTGTGAGCTGTCTAGCAATACGATA
ACGGAGCTATCACCTTCACTTTAAAGACTGGAGCTTACAAAGCTGACACTGTCA
TCCAATCCTCTTATGTTACTTCACAAAGCACCAGTTGAAGACTCTTAAACAACTTCACT
CTGACAGGGAAAGGATAGGATTTCAAAATAAACACAGGAATGTTCAACCCATGAAAG
AAATTTCTCACATTTCACAAAATCTGATACTGCTCTATGCTCCCATGTCGA
ATATGATATGCGCTTGGGAGCCATTCTTCATTTGGGACCTTGGCTAACATATC
CTCAGAAATTGCTGGGTTATAGCTTCAATTACCTGCTTGGAAATCTTGTGCTT
GGCATGAGATCTTCATTAAGCTGAAAATACAACACTCAGCTATGTCATCAAATCCTT
TGTGCTGATGGCTGATGGGTGTTACTGTCTTGTGGCATTTGCGATATAAAA
TACCGAGGGCAGTATCAGAACTGCTTGTGGATGAGAGGGTGCAGTGGCGCCTC
ATGGGGTTCTGGCCATGCTGTCACCGAAGTCTGCTGCTACTGACACTACTTGACT
TTGGAGAGTTCTGGTCAATTGCTTCCCCTCACTAACATTGACCTGAAAACCGCGAG
ACCTCAGTCATCCTCATTTGATCTGGATGGCGGGATTTTAAATGCTGAAATCCATT
TGGAAATAAGGATTATTGGAAACTTTATGGGAAAATGGAGATGTGTTCCCACTTTAT
TATGACCAAAACAGAGATATTGGAAAGGGATTCTCTGGAAATTTTGGAGAGGGTGGCTGTC
AACTTGCTGGCTTCTCATATTGTTCTCTATATTACTATGTTCTGTCATTCAA
AAAACGCCCTGGAGACCCACAGAACTGAGGATTGTTGGAGAGGGTGGCTGTC
AATGTTCTTTTATAGTGTCTGATGCCACTGCTGGATTCTGTATTGAGTT
AAAATCCCTTCCCTTCGGGTGGAAACACAGACACATGACTTCCCTGGATAGTGATT
TTTTCCTCCAGTTAACAGTGTGCTTGAATCCAATCTCATACTCTCACACCAACTTT
TTAAGGACAAGTTGAACACAGCTGCTGACAACACATGAGGGAAATCAATTCTCAAATT
AAAAAAAGTTTATCACATCATTGTTGTGGATAGAGGGACTCTCTTCCCTGAAACATT
GGGTTTGAACAAAATAACACTGGAGACAGTATAATGAAACAGTTCTCTAG

FIG.2

MFPLLLHFIVLINVQDFALTQGSMITPSCQKGYFFCGNLTKCLPRAFHCDGKDCCNGADE
ENCGDTSGWATIFGTVHGNANSVALTQECPFLKQYPQCCDCCKETELECVNGDLKSVPMLSN
NVTLLSLKKNKTHSLPDKVFIFYTKLKKIPLQHNCIRHISRKAFFGLCNLQILYLNHNCI
TTLRPGIFKDLHQLTWLILDDNPITRISQRLLFTGLNSLFFLSMVNNYLEALPKQMCQAQMP
QLNWVDLLEGNRIRKYLTNSTFLSCDSLTVLFLPRNQIOFVPEKTFSSLKNLGELDLSSNTI
TELSPLHLFKDLKLQKLNLGSNPMLMYLHKNQFESLKQLQSLDLERIEIPNINTRMFQPMK
NLSHIYFKNFRYCSYAPHVRICMPLTDGJISFEDLLANNILRIFVWWIAFITCFGNLFVI
GMRSFIKAENTTHAMSIKILCCADCLMGVVLFFVGIFDIKYRGQYQKYALLWMESVQCRL
MGPLAMLSTEVSVLLLTLYLLEKFLVIVVFFPSNIRPGKQRQTSVILICIWMAGLJAVIPF
WNKDYFGNFYGKNGVCFYYDQTEDIGSKGYSLGIFLGVNLLAFLIIIVFSYITMPCSIQ
KTALQTTEVRNCFGREVAVANRFFFIVFDAICWIPIVFFVKILSLFRVEIPDTMTSWIVI
FFLPVNSALNPILYLTITTNFFKDKLKQLHKHQRKSIFKIKKSLSTSIVWIEDSSLKL
GVLNKTTLGDSIMKPVS

FIG. 3

CCACGGCTCCGATTACA

09965536 - 092601

FIG. 4

CAATCATTGGATCACTGGACTTTCAGTGACTACCTAAACAGGGGACAGCTTTGGA
AGATGACATCTGCAATGCTTTCATCTTACCAACGGCAAGCTTCTGCACAGAGAGCA
CAGCAGAATGGCTCCGTCACTGCATTCACATGGCACTGTACTATCTACCAACCGTGT
GAGGACAGCACCAAAGGTTCTCTCTCACCACATGCTGAAAAGCACATGTGAATTG
GTGATAGTGGCTGAGGTGCACTGATCTAGCTAACACAACCCACAAAT
GACCACAGTTGCCACTGTGTGGTCTTCACATGGGTTGCACTGTCCATGAAAATGAAA
CACTCACACATCTGATTCAGTGTGGCCATAATAACAGAAATCTAACAACTCTTCC
GCCCTTCAATATCAAAATAACCCATCAGCATCTGCTGGATTGATAGCAAAAGGATTCC
AAAATATTCTACCGAAGTCTCTCTGTGAAGGCCGCTGGAGTAGCCACTTTGAAA
ACAGAACTTCCAACCGGTTACCATGCTAACCTATGACCAAGAGATCACACTGATGAAG
CCTCATACCATTGCTTGGATTATTAATATCAGAAGAGATGAATTCTAAGATA
TTTTCTGAAGGTGCCCCAGGGCACAAACAAATTGGACACTTCACTGCTAAAAAGTACA
CTTTAATATTCTAAAGATAATTCTTAGAGCAGTATCCTTATTGCTGGCAAGTCTG
CTTCATAAAATATGCGAGATAAGAAGTGTAAATGGGATTCAAGAAATTATGGTTTTATT
GGGACTGTTTGATACATCACAATGGTTTGTCTCATTTAACAAAAAAAGCAATGA
AGTTGGGGTGGTTTTGAAAACGAAACTGAAAAAAATTATATGTGAAAATGAGAACTG
GGTAAATAAAATTATATTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAG

FIG. 5

ATGTTCTTCTACTCATTCATCGTCTGATCAATGTCAAAGAATTTCGACTGACTCAA
 GGTAGCATGATCACTCCCTCATCCAAAAGGAATTTCCTGTGGGAACGGGGCGGACGAA
 TGCTTACCCGAGCTTTCACTGTGATGGCAAGGATGACTGTGGGAACGGGGCGGACGAA
 GAGAACCTGTGGGACACTAGTGATGGCGACCATAATTGGCACAGTGCATGGAAATGCT
 AACAGCGTGGCTTAACACAGGAGTGTCTTAAACAGTATCACCAATGCTGTGACTGC
 AAAGAACACTGAATTGGAAATGTGAAATGTGACTTAAAGTCTGTGCCGATGATTCTAAC
 AATGTGACATTACTGTCTTAAAGAAAAAAACAAATCCACACTCTCCAGATAAAAGTTTC
 ATCAAAATACACAAAACCTAAAGAATTTCCTCAGCATAATTGCAATTAGACACATATCC
 AGGAAAGCATTTTGGATTGTAAATCTGAAATATTAACTTCTAGATGACAAATCCAATA
 ACCAGAATTTCACAGCGCTGTTACGGGATAAAATTCTGTGTTTCTGTATGGTT
 AATAACTACTTAAAGCTCTCCAAAGCAGATGTGTGCCAAATGCCCTCAACTGTG
 GTGGATTGGAGGCAATAAGAATTACTCACAACATTACGTTCTGCGAT
 TCGCTCACAGTGTGTTCTGCCAGAAATCAATTGTTTGTGTTCCAGAGAGACATT
 TCTCTTAAAGAATTAGGAGAACCTGATCTGCTAGCAATACGATAACCGAGCTATCA
 CCTCACCTTAAAGACTGAGCTTCACAAAGCTGAAACCTGTCAATCCAACTCTT
 ATGTAATCTCACAAGAACCTGTTGGAAAGCTTAAACAACTTCAGTCTGACACTGAA
 AGGGAGAGATTCCAAATAACACACGAACTGTTCAACCCATGAAGAATTCTC
 ATTATTTCAAAACTTCGATGCTCTTATGCTCCCCTATGTCGAATATGTATGCC
 TTGACGGACCGCATTTCTCATTTGAGGACCTTGGCTAACATATCCTCAGAATATT
 GTCTGGTTATGCTCTTACCTGTTGGAAATCTTTGTGATGGCATGAGATCT
 TTCAATTAAAGCTGAAAAATCAACCTCACGGCTATGTCATCATAAATCTTGTGCTGAT
 TGCCTGATGGGTGTTACTTGTCTTGTGCTATTTGCAATATAAAACCGAGGGCAG
 TATCAGAAAGTATGCCCTGCIGTGATGGAGAGCCTGCACTGGCCCTCATGGGGTTCTG
 GCCATCTGTCACCGGAAGTCTCTGCTCTGACTGACCTACTTGAATTGGAGAAGTT
 CTGTCATTTGATCTCCCCCTCAGTAAACATTGCACTGAAACGGCAGACCTCAGTCATC
 CTCATTGATCTGGATGGGGATTTTAATAGCTGAACTTCCATTGGATAAAGGAT
 TATTGGAAACATTGAAAGGATGAGTATGTTCCACTTTATATGACAAACA
 GAAGATATTGGAAAGCAAAAGGTTATCTCTTGGAAATTTCCTAGGTGTGAACTTGCTGGCT
 TTCTCATCATTGTTCTTCTTAAATTACTATGTTCTGTTCCATTAAAAACCGCCTG
 CAGACACAGAAGTAAGAATTGTTGGAGAGAGGTGGCTGTCGAAATGTTCTT
 TTATAGTGTCTCTGATGCCATTGCTGGATTCTGTTGAGTAAATGTTGAGTAA
 CTCTCCGGGTGAAATACAGACACATGACTTCTGATAGTATTTTCTTCCA
 GTAAACAGTGCTTGGATCAATCCTCTATACTCTCACACCAACTTTTAAGGACAAG
 TTGAAACAGCTGTCGACAAACACATCAGAGGAATCAATTTCAAAATTTAAAGT
 TTATCTACATCCATTGTTGGATAGAGGACTCTCTTCCCTGAAACTGGGTTTGAAAC
 AAAATAACACTGGAGACAGTATAATGAAACAGTTCTAG

FIG. 6

MFLLLHFIVLINVKDFALTQGSINITPSQCQGYFCGNLTCKLPRAFHCDGKDGCNGADE
ENCGDTSGWATIFGTVHGNANSVALTQECFLKQYQPQCCDCETBLECVNGDLKSVPMSN
NVTLLSLKKNNKIHSLPDVKFIKYTKLKKFLQHNCIRHISRKAFFGLCNLQILILDDNP
TRISQRFLTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGNRKYLTNSTFLSCD
SLTVLFLPQRQIGFVEPKTFSSLKNLGEELLSNTITELSPHLFKDLKLQKLNLSSNPL
MYLHNQFESLKQIQLSLDLERIEIPNINTRMFQPMKNSHIIYFKNFRYCSYAPHVRICMP
LTDGISSFEDLLANNILRIFVWVIAFCGNLFVIGMRSPIKAENTTHAMSIKILCCAD
CLMGVYLFVGIFDIKYRGQYQKAYALLWMESVQCRLMGFLAMLSTEVSVLLLTYLTLEKF
LVIIVFPFSNIRPGKRTSVLICIWMAFLVIAFWNPKDQFGNFYKGNGVCFPLYYDQT
EDIGSKGYSLGFLGVNLLAFLIIVMFCSIQKTAQTTTEVRNCFGREVAANRPF
FIVFSDAIWCIPVFVVKILSLFRVEIPDMTSWIVIFFLPVNSALNPILYLTTLTNFFKDK
LKQLLHKHQRKSIFKIKKSLSTSIVWIEDSSSLKGLVNLKITLGDSIMKPVS

FIG. 7

MFLLLHFIVL INVKDFALTQ GSINITPSQCQ GYFCGNLTCKLPRAFHCDGKDGCNGADE
KDDCGNGADE ENCGDTSGWA TIFGTVHGNNA NSVALTQECF LKQYQPQCCDC
KETELECVNG DLKSVPMSN NVTLLSLKKN KIHSLPDVKF IKYTKLKKLF
LQHNCIRHIS RKAFFGLCNL QILYLNHCNI TTLRPGIFKD LHQLTWLILD
DNPITRISQR LFTGLNSLFF LSMVNNEYLA LPKQMCAQMP QLNWVDLEG
RIKYLTNSTF LS CDSLITVLF LPRRNQIGFVP EKTFSSLKNL GELDLSSNTI
TELSPHLFKD LKLQQLNLS SNPLMLYHKN QFESLKQLOS LDLERIEIPN
INTRMFQPMK NL SHIYFKNF RYCSYAPHVR ICMLPTDGIS SFEDLLANNI
LRIFVWVIAF **ITCFGNLFVI GMRSPIKAEN TTHAMSIKIL CCACDLMGVY**
LFFFVGIEDIK YRGQYQKYL LMVESVOCPL MGFLAMLSTE VS VLLLTLYLT
LEKFLVIVFP FSNIRPGKRT SVLICIWAGFLIAVIFP WNKDYFGNFY
GKNGVCFPLY YDQTEDIGSK GYSLGFLGV NLLAFLIIVF SYITMFCSIQ
KTALQTTTEVR NCFCGREVAVA NR **FFFIVFSD AICWIPVFVVK ILSLFRVEI**
PDTMTS **WIVI FFLPVNSALN PILYLT TNF FDKLKQLLKH KHQRKSIFKI**
KKKSLSTSIV WIEDSSSLKL GVNLKITLGD SIMKPVS

FIG. 8A

HGPRBMY5	-----
HGPRBMY5_splice	-----
GPCR_LYMST	MATMSGTTIVCLIYLTTMLGNNSQGVNLKIESPSPPTLCSVEGTFFHCDGM
FSHR_RAT	-----
Q64183	-----
FSHR_EQUAS	-----
FSHR_CHICK	-----
LSHR_CALJA	-----
O75473	-----
HGPRBMY5	-----
HGPRBMY5_splice	-----
GPCR_LYMST	DQCVLIMGSKCDGVSDCEGMDESVETCGCLQSEFQCNHTTCIDKILRCDR
FSHR_RAT	-----
Q64183	-----
FSHR_EQUAS	-----
FSHR_CHICK	-----
LSHR_CALJA	-----
O75473	-----
HGPRBMY5	-----
HGPRBMY5_splice	-----
GPCR_LYMST	NDDCSNGLDERECDIYICPLGTHVKWHNHFcvPRDKQDFLDDCGDNSDE
FSHR_RAT	-----
Q64183	-----
FSHR_EQUAS	-----
FSHR_CHICK	-----
LSHR_CALJA	-----
O75473	-----
HGPRBMY5	-----
HGPRBMY5_splice	-----
GPCR_LYMST	KICERRECVATEFKCNNSQVAFGNLCDGLVDCVDGSDEDQVACDSDKYF
FSHR_RAT	-----
Q64183	-----
FSHR_EQUAS	-----
FSHR_CHICK	-----
LSHR_CALJA	-----
O75473	-----
HGPRBMY5	-----
HGPRBMY5_splice	-----
GPCR_LYMST	QCAEGSLIKKEFVCDGWVDCKLTFADELNCKLCDEDDFRCSDTRCIQKSN
FSHR_RAT	-----
Q64183	-----
FSHR_EQUAS	-----
FSHR_CHICK	-----
LSHR_CALJA	-----
O75473	-MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRG
HGPRBMY5	-----
HGPRBMY5_splice	-----
GPCR_LYMST	VCDGYCDOCCTCDDEEVCANNTYGCPMDTKYMCRSIYGEPRCIDKDNCNM

09965536 - 092501

FIG. 8B

FIG. 8C

FSHR_CHICK LSHR_CALJA 075473	DIEKIEISONDALIIEEGNUSSLEKHLBIRIEKANKUMKUDODAFHOL EVIKI. EISOSDLSLERIENAGANDNLUNNLSITLONTKNIHIEHGARTN SUTI. HFYDNP. IQFVGSRASQHBEELRTTNGSOTTEF. HD. LTGT
HGPRBMY5 HGPRBMY5_splice GPCR_LYMLST FSHR_RAT Q64183 FSHR_EQUAS FSHR_CHICK LSHR_CALJA 075473	CNLQIYENHNCGITTERPGLFKDHQI. TWLILD. DN. PITRISQRFL. CNLQI. DILD. DN. PITRISQRFL. COCGCVTMDCTGQKLKEMPVQVQMEEDL. SKEMIG. DN. LLNLTTTFS PSLRYLILSNTGIL-ELP. AVHVKLQSLO. KVLLIDICODINNIHIVARNSFM PSLRYLILSNTGIL-ELP. AVHVKLQSLO. KVLLIDICODINNIHIVARNSFM PSLRYLILSNTGIL-ELP. AVHVKLQSLO. KVLLIDICODINNIHIVARNSFM PSLRYLILSNTGIL-ELP. AVHVKLQSLO. KVLLIDICODINNIHIVARNSFM PSLRYLILSNTGIL-ELP. AVHVKLQSLO. KVLLIDICODINNIHIVARNSFM PSLRYLILSNTGIL-ELP. DVHNLPSSETNFIT. ETCDNLHTTTEPIQAFQ PRKYLISLNTGIRKPF. DVHNLPSSETNFIT. ETCDNLHTTTEPIQAFQ ANLESITLTGAQISSLPLQPTVCNQEPNPLQ. . VLDLSESYL. LEDDLP. . SF.
HGPRBMY5 HGPRBMY5_splice GPCR_LYMLST FSHR_RAT Q64183 FSHR_EQUAS FSHR_CHICK LSHR_CALJA 075473	. TGLNDLFFPLSMVNYYIEBALPKQCMCAQMPOLNWDDLGQN. RIKYLINTSF . TGLNDLFFPLSMVNYYIEBALPKQCMCAQMPOLNWDDLGQN. RIKYLINTSF ATYYDKVTYLDIENRNHETIPIYPSFONMWLTHLNLDNM. NETSLKGNSL GUSFESVI. LWSLNGKJIEETHNQAFNG. TOLDPELNLSDNNNLBBLPNDVF GUSFESVI. LWSLNGKJIEETHNQAFNG. TOLDPELNLSDNNNLBBLPNDVF GUSFESVI. LRLNNGKJIEBKHDHFNG. TOLDPELNLSDNNNLBBLPNDVF GUSFESVI. LKLYGNQFEEVQSHAFNG. ITVVISLVIKENVHLBRHNGAP SVCQKLQK. IDRHNHPIEYIKVDTFCQQLSLRSLSNLAWN. KIAIIHPNAF
HGPRBMY5 HGPRBMY5_splice GPCR_LYMLST FSHR_RAT Q64183 FSHR_EQUAS FSHR_CHICK LSHR_CALJA 075473	LSCDSLTLDFPLPNQGFPPEKTFSSLKNGEGLDLSSNTTTELSEPHKFD LSCDSLTLDFPLPNQGFPPEKTFSSLKNGEGLDLSSNTTTELSEPHKFD LQLSLNKOIIINGNKUETIEEDFTSSMTPVTLVDDLSNQPOTHVYKNMNGK QGASGEVWLDISRTKVHSPLNEGLELNKKURKA. RSTYRPLKKL. PNLDKF QGASGEVWLDISRTKVHSPLNEGLELNKKURKA. RSTYRPLKKL. PNLDKF QGASGEVWLDISRTKVHSPLNEGLELNKKURKA. RSTYRPLKKL. PSLBKF QGASGEVWLDISRTKVHSPLNEGLELNKKURKA. RSTYRPLKKL. PDVNLKF RGAGGSELDISSTKQALSHGLESITQTHIA. TSSYSLKKL. DSREKF STLPLSIIMLD. BSNLNLSSEFIIGLHGTHKL. TGNAHQSL. ISSENFE
HGPRBMY5 HGPRBMY5_splice GPCR_LYMLST FSHR_RAT Q64183 FSHR_EQUAS FSHR_CHICK LSHR_CALJA 075473	LNLQ. PLNLSSENPLMLYH. KNPFESKQLOSLDLEIEIPNINTRMPQP LNLQ. PLNLSSENPLMLYH. KNPFESKQLOSLDLEIEIPNINTRMPQP LKOIT. VLNISRNQINSID. NGAFNNCANVRLIDESGNVHINDIQGVKVFMG VLMEMSLTYPSHCCAAFAANLKROISEHPCNKSILRQD. DMTOQDGR VLMEMSLTYPSHCCAAFAANLKROISEHPCNKSILRQD. DMTOQDGR VLMEMSLTYPSHCCAAFAANLKROISEHPCNKSILRQD. DMTOQDGR RSLLIEADTYPSHCCAAFAANLKROISEHPCNKSILRQD. DMTOQDGR RSLLIEADTYPSHCCAAFAANLKROISEHPCNKSILRQD. DMTOQDGR RSLLIEADTYPSHCCAAFAANLKROISEHPCNKSILRQD. DMTOQDGR PEUKVIEPMYIYCCAF. GVCENAYKTISQNWNKGD. NSSMDL. HKKDAG
HGPRBMY5 HGPRBMY5_splice GPCR_LYMLST FSHR_RAT Q64183 FSHR_EQUAS FSHR_CHICK LSHR_CALJA 075473	MKNL. SHYFKNFRY. CSYAPHVRICMLTDGCISSFEDLIA MKNL. SHYFKNFRY. CSYAPHVRICMLTDGCISSFEDLIA EPLR. VEKTDTSYRF. COLAPECVCSPSKPOBCFSSCEDIMS VSLIDESPS. YGKGSDMMNMFYD. LQNEVWVDCSCKPDAPNPCEDEDIMG VSLIDESPS. YGKGSDMMNMFYD. LQNEVWVDCSCKPDAPNPCEDEDIMG VSLIDESPS. MMYSSEFYD. LQNEVWVDCSCKPDAPNPCEDEDIMG RSAABDYISHYGRFGVENEFDYDGLONEVWDFVCSKPDAFNPCEDIMG DYPFAFAESGSG. DWDYGF. HLKPTKPCAAPEPDAFNPCEDIMG MFOAOE. DRDLEDFLDDE. KALHLSVCSOCS-PGEPIPECHEHLD

Fig. 8D

HGPRBMY5	NNILRFFWWIAFIFTCGFLVIGMRSFIKAENIATHMSIKLCCGCLM
HGPRBMY5_splice	NNILRFFWWIAFIFTCGFLVIGMRSFIKAENIATHMSIKLCCGCLM
GPCR_LY MST	NHVLRLSVIWWGVLFVGVFWPFVWRVRDPRFGKXHSPLTNTLICDFLM
FSHR_RAT	YNILRLRVLWISILALAITGTNTIVLTLISQYKLTVPRFLMCNLAFADECE
Q64183	YNILRLRVLWISILALAITGTNTIVLTLISQYKLTVPRFLMCNLAFADECE
FSHR_EQUAS	YDILRLRVLWISILALAITGTNTIVLTLISQYKLTVPRFLMCNLAFADECE
FSHR_CHICK	YDILRLRVLWISILALAITGTNTIVLTLISQYKLTVPRFLMCNLAFADECE
LSPHR_CALJA	YDILRLRVLWISILALAITGTNTIVLTLISQYKLTVPRFLMCNLAFADECE
075473	YDILRLRVLWISILALAITGTNTIVLTLISQYKLTVPRFLMCNLAFADECE
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HGPRBMY5	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
HGPRBMY5_splice	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
GPCR_LY MST	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
FSHR_RAT	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
Q64183	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
FSHR_EQUAS	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
FSHR_CHICK	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
LSPHR_CALJA	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
075473	GIVLFFVGIFD1KYMGGQYQKVALIWMESVCOORLNGFLAMLSIENSVLLT
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HGPRBMY5	YITLLEGLVIVFPFNS.NIRPGKQRTSIVLICINNAGLILAIIPFWNKQDYF
HGPRBMY5_splice	YITLLEGLVIVFPFNS.NIRPGKQRTSIVLICINNAGLILAIIPFWNKQDYF
GPCR_LY MST	TITLELICILFPLR.RTRIGLQLQAIIVMSCIINLVPLAIALPPLIGFSVF
FSHR_RAT	ATTLERWHTITHMQECKVQLRHAASVNVILGWAEAAALGFPIRGGISS.
Q64183	ATTLERWHTITHMQECKVQLRHAASVNVILGWAEAAALGFPIRGGISS.
FSHR_EQUAS	ATTLERWHTITHMQECKVQLRHAASVNVILGWAEAAALGFPIRGGISS.
FSHR_CHICK	ATTLERWHTITHMQECKVQLRHAASVNVILGWAEAAALGFPIRGGISS.
LSPHR_CALJA	ATTLERWHTITHMQECKVQLRHAASVNVILGWAEAAALGFPIRGGISS.
075473	ATTLERWHTITHMQECKVQLRHAASVNVILGWAEAAALGFPIRGGISS.
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HGPRBMY5	GNFYGNGVQCPPIYYDQTEDIGSKGSIIGIFLGNLALAFELIVFSYIITME
HGPRBMY5_splice	GNFYGNGVQCPPIYYDQTEDIGSKGSIIGIFLGNLALAFELIVFSYIITME
GPCR_LY MST	ENFYGRSGVCLAHVTPDRRGWNE.MSCVGFFILLNLSFVIIASSYVME
FSHR_RAT	...YMKVSIICLPMID1SPL...SOLYIPLLLU..LNVLVAFVVICGCCYTHIY
Q64183	...YMKVSIICLPMID1SPL...SOLYIPLLLU..LNVLVAFVVICGCCYTHIY
FSHR_EQUAS	...YMKVSIICLPMID1SPL...SOLYIPLLLU..LNVLVAFVVICGCCYTHIY
FSHR_CHICK	...YMKVSIICLPMID1SPL...SOLYIPLLLU..LNVLVAFVVICGCCYTHIY
LSPHR_CALJA	...YMKVSIICLPMID1SPL...SOLYIPLLLU..LNVLVAFVVICGCCYTHIY
075473	...YMKVSIICLPMID1SPL...SOLYIPLLLU..LNVLVAFVVICGCCYTHIY
<hr/>	
HGPRBMY5	CSIQKT..ALQTEEVRCFCGREVAVANFFFIVPSDADCIWIPFVVKLILS
HGPRBMY5_splice	CSIQKT..ALQTEEVRCFCGREVAVANFFFIVPSDADCIWIPFVVKLILS
GPCR_LY MST	SVAKKTRSAVRTEAESN..DNAMAPRMTIVNDFCOPAPIVILGVFS
FSHR_RAT	LIVRNNTETVSSSSDTK.....IAKRMATLIFTDPCMAPISFFPISI
Q64183	LIVRNNTETVSSSSDTK.....IAKRMATLIFTDPCMAPISFFPISI
FSHR_EQUAS	LIVRNNTETVSSSSDTK.....IAKRMATLIFTDPCMAPISFFPISI
FSHR_CHICK	LIVRNNTETVSSSSDTK.....IAKRMATLIFTDPCMAPISFFPISI
LSPHR_CALJA	FAVRNENVISSNDTCK.....IAKRMATLIFTDPCMAPISFFPISI
075473	FAVRNENVISSNDTCK.....IAKRMATLIFTDPCMAPISFFPISI
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FIG. 8E

HGPRBMY5	LFRME. IPDNTMSWIVVIFLPNGSALNPILYLTINFFKDKLKQOLHHHQ
HGPRBMY5_splice	LFRME. IPDNTMSWIVVIFLPNGSALNPILYLTINFFKDKLKQOLHHHQ
GPCR_LYMST	LAGAR. ADDOYVAWII. FVLPNNSATNPVWYTISTLPLFLGNVRKRANRPR
FSHR_RAT	SILWPLITVSKAKELLVLFYPINSCANPFLYAIFTMIFRRDFEILLSKFG
Q64183	SILWPLITVSKAKELLVLFYPINSCANPFLYAIFTMIFRRDFEILLSKFG
FSHR_EQUAS	SILWPLITVSKAKELLVLFYPINSCANPFLYAIFTMIFRRDFEILLSKFG
FSHR_CHICK	SILWPLITVSKAKELLVLFYPINSCANPFLYAIFTMIFRRDFEILLSKFG
LSHR_CALJA	AFKMPPLITVTSKVLVLFYPINSCANPFLYAIFTMIFRRDFEILLSKFG
O75473	LINUTPLISPEVIKFTLIVVVPIPAGLNPDLYLIFNPNPHFED. LVSARK..
 HGPRBMY5	RKSIFKII...KKKSL...SISIVWIEDSSSLKLGVLNKI.TLGDS. IMKP
HGPRBMY5_splice	RKSIFKII...KKKSL...SISIVWIEDSSSLKLGVLNKI.TLGDS. IMKP
GPCR_LYMST	KSFTHSFTGDTKH\$YVDDGCTTHSYCEKKSPYRQLELKRLRSLNSS...PP
FSHR_RAT	QYEQO.QIY.RTEETSS..ATHNFHARKSHCSSLAPR...VIN..SYVLLVP
Q64183	QYEQO.QIY.RTEETSS..ATHNFHARKSHCSSLAPR...VIN..SYVLLVP
FSHR_EQUAS	QYEQO.QIY.RTEETSS..TGHISHP\$NGPCPTTPR...VINGANCILVP
FSHR_CHICK	QCERO.QIY.RTEETSS..SAHNFHTRNGHYPTASK...NSDGTIYSLVP
LSHR_CALJA	CKHRRELY.RRKDFG..A.YTSNYKNG.FTGSSK...PSQST..LKP
O75473CTYWWTBSKHPDSL\$INSDDVEKQSCDSTQALVTFTSSSITYDLP
 HGPRBMY5	VS-----
HGPRBMY5_splice	VS-----
GPCR_LYMST	MYNTTELHSDS-----
FSHR_RAT	LNHSQQN-----
Q64183	LNHSQQN-----
FSHR_EQUAS	LSHLAQN-----
FSHR_CHICK	LNHLN-----
LSHR_CALJA	ALHCOGTALLDKTCYKEY-----
O75473	SSVPSPAYPVTE SCHLSSVA FVPCL

FIG. 9A

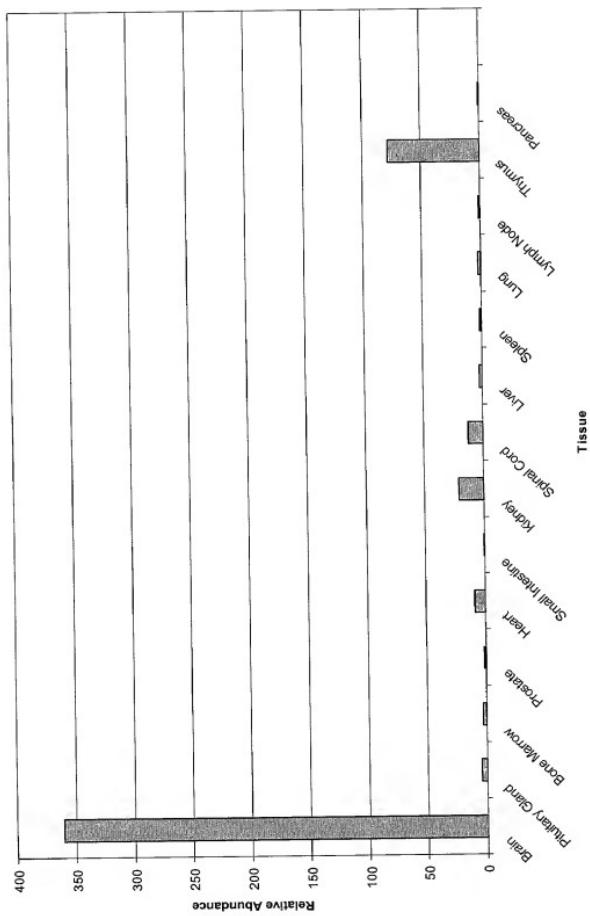
1 MFPLLHFIVLINVKDFALTQGSMITPSCQKGYFCGNLTKCLPRAFHCDG 50
 |||||||
 1 MFPLLHFIVLINVKDFALTQGSMITPSCQKGYFCGNLTKCLPRAFHCDG 50
 |||||||
 51 KDDCGNGADEENCQDTSGWATIFGTVHGNANSVALTQECKLQYPCQCCDC 100
 |||||||
 51 KDDCGNGADEENCQDTSGWATIFGTVHGNANSVALTQECKLQYPCQCCDC 100
 |||||||
 101 KETELECVNGDLKSVPMSNNVTTLSLKKNIHSPLDKVFIKYTKLKKIF 150
 |||||||
 101 KETELECVNGDLKSVPMSNNVTTLSLKKNIHSPLDKVFIKYTKLKKIF 150
 |||||||
 151 LQHNCIRHSRKAPFGLCNLQIILYLNHNCITTLRPGIPKDLHQQLTWLILD 200
 |||||||
 151 LQHNCIRHSRKAPFGLCNLQI.....LILD 176
 |||||||
 201 DNPITRISQRLLPTGLNSLFFLMSMVNNYLEALPKQMCACQMPQLNWNVDLEGN 250
 |||||||
 177 DNPITRISQRLLPTGLNSLFFLMSMVNNYLEALPKQMCACQMPQLNWNVDLEGN 226
 |||||||
 251 RIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI 300
 |||||||
 227 RIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI 276
 |||||||
 301 TELSPHLFKDLKLQLKLNLSNPLMLYHKNQFESLKQLQSDLRERIEIPN 350
 |||||||
 277 TELSPHLFKDLKLQLKLNLSNPLMLYHKNQFESLKQLQSDLRERIEIPN 326
 |||||||
 351 INTRMFQPQPMNLSHIYFKNFRCYCSYAPHVRICMPLTDGISSFEDLLANNI 400
 |||||||
 327 INTRMFQPQPMNLSHIYFKNFRCYCSYAPHVRICMPLTDGISSFEDLLANNI 376
 |||||||
 401 LRIFWVVIAPITCFGNLFVIGMRSFIKAENTTHAMSIKILCCADCLMGVY 450
 |||||||
 377 LRIFWVVIAPITCFGNLFVIGMRSFIKAENTTHAMSIKILCCADCLMGVY 426
 |||||||
 451 LFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLTYLT 500
 |||||||
 427 LFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLTYLT 476
 |||||||
 501 LEKFLVIVFPFSNIRPGKRQTSVILICIWMMAGFLIAVIPFWNKDYFGNFY 550
 |||||||
 477 LEKFLVIVFPFSNIRPGKRQTSVILICIWMMAGFLIAVIPFWNKDYFGNFY 526
 |||||||
 551 GKNGVCFPPLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIIVFSYITMFCSIQ 600
 |||||||
 527 GKNGVCFPPLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIIVFSYITMFCSIQ 576

FIG. 9B

601 KTALQTTEVRNCFGREVAVANRFFIVFSDAICWIPVFVVKILSLFRVEI 650
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
577 KTALQTTEVRNCFGREVAVANRFFIVFSDAICWIPVFVVKILSLFRVEI 626
||||| ||||| ||||| ||||| ||||| ||||| |||||
651 PDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLQQLLHKHQRKSIFPKI 700
||||| ||||| ||||| ||||| ||||| ||||| |||||
627 PDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLQQLLHKHQRKSIFPKI 676
||||| ||||| ||||| ||||| ||||| |||||
701 KKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPV 737
||||| ||||| ||||| ||||| ||||| |||||
677 KKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPV 713
||||| ||||| ||||| ||||| |||||

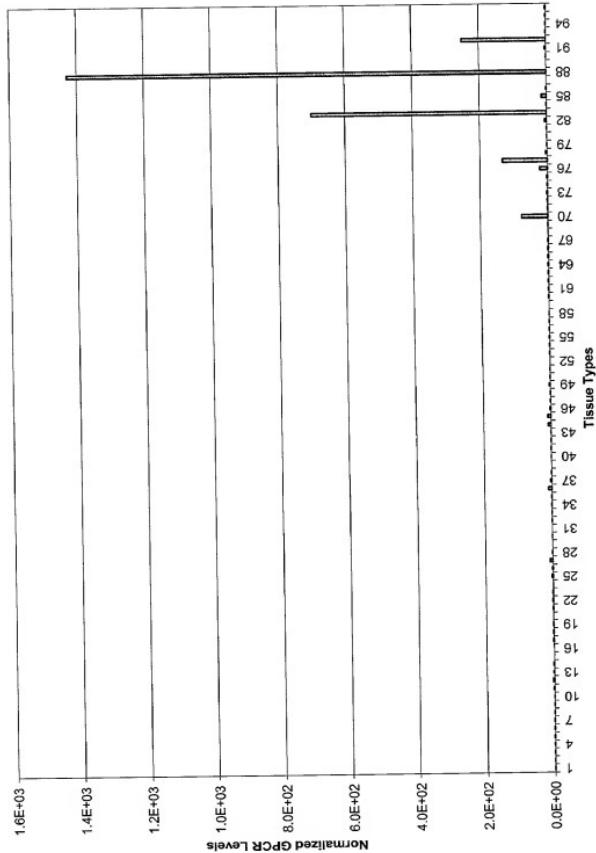
00-55555560-02522901

FIG. 10



0109296 " 3555660

FIG. 11



T09260" 9555660

FIG. 12

